



IFWO

RAW SEQUENCE LISTING

DATE: 09/16/2004

PATENT APPLICATION: US/10/776,604

TIME: 15:51:55

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\09162004\J776604.raw

5 <110> APPLICANT: Shimizu, Nobuyoshi
 6 Mizuno, Yoshikuni
 9 <120> TITLE OF INVENTION: DNAs or Genes Participating in Parkinson's Disease
 12 <130> FILE REFERENCE: 0652.2110001
 15 <140> CURRENT APPLICATION NUMBER: 10/776,604
 16 <141> CURRENT FILING DATE: 2004-02-12
 19 <150> PRIOR APPLICATION NUMBER: 09/601,844
 20 <151> PRIOR FILING DATE: 2000-08-09
 23 <150> PRIOR APPLICATION NUMBER: PCT/JP99/00545
 24 <151> PRIOR FILING DATE: 1999-02-09
 27 <150> PRIOR APPLICATION NUMBER: JP 10/27531
 28 <151> PRIOR FILING DATE: 1998-02-09
 31 <160> NUMBER OF SEQ ID NOS: 70
 34 <170> SOFTWARE: PatentIn version 3.1
 38 <210> SEQ ID NO: 1
 40 <211> LENGTH: 2960
 42 <212> TYPE: DNA
 44 <213> ORGANISM: Homo sapiens
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 50 <221> NAME/KEY: CDS
 52 <222> LOCATION: (102)..(1496)
 54 <223> OTHER INFORMATION:
 58 <220> FEATURE:
 60 <221> NAME/KEY: misc_feature
 62 <222> LOCATION: (102)..(108)
 64 <223> OTHER INFORMATION: Exon 1
 W--> 68 <220>
 70 <221> NAME/KEY: misc_feature
 72 <222> LOCATION: (109)..(272)
 74 <223> OTHER INFORMATION: Exon 2
 78 <220> FEATURE:
 80 <221> NAME/KEY: misc_feature
 82 <222> LOCATION: (273)..(513)
 84 <223> OTHER INFORMATION: Exon 3
 88 <220> FEATURE:
 90 <221> NAME/KEY: misc_feature
 92 <222> LOCATION: (514)..(635)
 94 <223> OTHER INFORMATION: Exon 4
 98 <220> FEATURE:
 100 <221> NAME/KEY: misc_feature
 102 <222> LOCATION: (636)..(719)
 104 <223> OTHER INFORMATION: Exon 5
 108 <220> FEATURE:

(pg. 6)

ENTERED

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112 <222> LOCATION: (720)..(835)
114 <223> OTHER INFORMATION: Exon 6
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122 <222> LOCATION: (836)..(972)
124 <223> OTHER INFORMATION: Exon 7
128 <220> FEATURE:
130 <221> NAME/KEY: misc_feature
132 <222> LOCATION: (973)..(1034)
134 <223> OTHER INFORMATION: Exon 8
138 <220> FEATURE:
140 <221> NAME/KEY: misc_feature
142 <222> LOCATION: (1035)..(1184)
144 <223> OTHER INFORMATION: Exon 9
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150 <221> NAME/KEY: misc_feature
152 <222> LOCATION: (1185)..(1268)
154 <223> OTHER INFORMATION: Exon 10
158 <220> FEATURE:
160 <221> NAME/KEY: misc_feature
162 <222> LOCATION: (1269)..(1386)
164 <223> OTHER INFORMATION: Exon 11
168 <220> FEATURE:
170 <221> NAME/KEY: misc_feature
172 <222> LOCATION: (1387)..(2960)
174 <223> OTHER INFORMATION: Exon 12
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181 gggcctgttc ctggcccgca gccgccacct acccagtac c atg ata gtg ttt gtc      116
182                                     Met Ile Val Phe Val
183                                     1          5
185 agg ttc aac tcc agc cat ggt ttc cca gtg gag gtc gat tct gac acc      164
186 Arg Phe Asn Ser Ser His Gly Phe Pro Val Glu Val Asp Ser Asp Thr
187          10          15          20
189 agc atc ttc cag ctc aag gag gtg gtt gct aag cga cag ggg gtt ccg      212
190 Ser Ile Phe Gln Leu Lys Glu Val Val Ala Lys Arg Gln Gly Val Pro
191          25          30          35
193 gct gac cag ttg cgt gtg att ttc gca ggg aag gag ctg agg aat gac      260
194 Ala Asp Gln Leu Arg Val Ile Phe Ala Gly Lys Glu Leu Arg Asn Asp
195          40          45          50
197 tgg act gtg cag aat tgt gac ctg gat cag cag agc att gtt cac att      308
198 Trp Thr Val Gln Asn Cys Asp Leu Asp Gln Gln Ser Ile Val His Ile
199          55          60          65
201 gtg cag aga ccg tgg aga aaa ggt caa gaa atg aat gca act gga ggc      356
202 Val Gln Arg Pro Trp Arg Lys Gly Gln Glu Met Asn Ala Thr Gly Gly
203 70          75          80          85
205 gac gac ccc aga aac gcg gcg gga ggc tgt gag cgg gag ccc cag agc      404
206 Asp Asp Pro Arg Asn Ala Ala Gly Gly Cys Glu Arg Glu Pro Gln Ser

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207		90		95		100	
209	ttg act cgg gtg gac ctc agc agc tca gtc ctc cca gga gac tct gtg						452
210	Leu Thr Arg Val Asp Leu Ser Ser Ser Val Leu Pro Gly Asp Ser Val						
211		105		110		115	
213	ggg ctg gct gtc att ctg cac act gac agc agg aag gac tca cca cca						500
214	Gly Leu Ala Val Ile Leu His Thr Asp Ser Arg Lys Asp Ser Pro Pro						
215		120		125		130	
217	gct gga agt cca gca ggt aga tca atc tac aac agc ttt tat gtg tat						548
218	Ala Gly Ser Pro Ala Gly Arg Ser Ile Tyr Asn Ser Phe Tyr Val Tyr						
219		135		140		145	
221	tgc aaa ggc ccc tgt caa aga gtg cag ccg gga aaa ctc agg gta cag						596
222	Cys Lys Gly Pro Cys Gln Arg Val Gln Pro Gly Lys Leu Arg Val Gln						
223	150		155		160		165
225	tgc agc acc tgc agg cag gca acg ctc acc ttg acc cag ggt cca tct						644
226	Cys Ser Thr Cys Arg Gln Ala Thr Leu Thr Leu Thr Gln Gly Pro Ser						
227		170		175		180	
229	tgc tgg gat gat gtt tta att cca aac cgg atg agt ggt gaa tgc caa						692
230	Cys Trp Asp Asp Val Leu Ile Pro Asn Arg Met Ser Gly Glu Cys Gln						
231		185		190		195	
233	tcc cca cac tgc cct ggg act agt gca gaa ttt ttc ttt aaa tgt gga						740
234	Ser Pro His Cys Pro Gly Thr Ser Ala Glu Phe Phe Phe Lys Cys Gly						
235		200		205		210	
237	gca cac ccc acc tct gac aag gaa aca cca gta gct ttg cac ctg atc						788
238	Ala His Pro Thr Ser Asp Lys Glu Thr Pro Val Ala Leu His Leu Ile						
239		215		220		225	
241	gca aca aat agt cgg aac atc act tgc att acg tgc aca gac gtc agg						836
242	Ala Thr Asn Ser Arg Asn Ile Thr Cys Ile Thr Cys Thr Asp Val Arg						
243	230		235		240		245
245	agc ccc gtc ctg gtt ttc cag tgc aac tcc cgc cac gtg att tgc tta						884
246	Ser Pro Val Leu Val Phe Gln Cys Asn Ser Arg His Val Ile Cys Leu						
247		250		255		260	
249	gac tgt ttc cac tta tac tgt gtg aca aga ctc aat gat cgg cag ttt						932
250	Asp Cys Phe His Leu Tyr Cys Val Thr Arg Leu Asn Asp Arg Gln Phe						
251		265		270		275	
253	gtt cac gac cct caa ctt ggc tac tcc ctg cct tgt gtg gct ggc tgt						980
254	Val His Asp Pro Gln Leu Gly Tyr Ser Leu Pro Cys Val Ala Gly Cys						
255		280		285		290	
257	ccc aac tcc ttg att aaa gag ctc cat cac ttc agg att ctg gga gaa						1028
258	Pro Asn Ser Leu Ile Lys Glu Leu His His Phe Arg Ile Leu Gly Glu						
259		295		300		305	
261	gag cag tac aac cgg tac cag cag tat ggt gca gag gag tgt gtc ctg						1076
262	Glu Gln Tyr Asn Arg Tyr Gln Gln Tyr Gly Ala Glu Glu Cys Val Leu						
263	310		315		320		325
265	cag atg ggg ggc gtg tta tgc ccc cgc cct ggc tgt gga gcg ggg ctg						1124
266	Gln Met Gly Gly Val Leu Cys Pro Arg Pro Gly Cys Gly Ala Gly Leu						
267		330		335		340	
269	ctg ccg gag cct gac cag agg aaa gtc acc tgc gaa ggg ggc aat ggc						1172
270	Leu Pro Glu Pro Asp Gln Arg Lys Val Thr Cys Glu Gly Gly Asn Gly						
271		345		350		355	

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273 ctg ggc tgt ggg ttt gcc ttc tgc cgg gaa tgt aaa gaa gcg tac cat      1220
274 Leu Gly Cys Gly Phe Ala Phe Cys Arg Glu Cys Lys Glu Ala Tyr His
275          360          365          370
277 gaa ggg gag tgc agt gcc gta ttt gaa gcc tca gga aca act act cag      1268
278 Glu Gly Glu Cys Ser Ala Val Phe Glu Ala Ser Gly Thr Thr Thr Gln
279          375          380          385
281 gcc tac aga gtc gat gaa aga gcc gcc gag cag gct cgt tgg gaa gca      1316
282 Ala Tyr Arg Val Asp Glu Arg Ala Ala Glu Gln Ala Arg Trp Glu Ala
283 390          395          400          405
285 gcc tcc aaa gaa acc atc aag aaa acc acc aag ccc tgt ccc cgc tgc      1364
286 Ala Ser Lys Glu Thr Ile Lys Lys Thr Thr Lys Pro Cys Pro Arg Cys
287          410          415          420
289 cat gta cca gtg gaa aaa aat gga ggc tgc atg cac atg aag tgt ccg      1412
290 His Val Pro Val Glu Lys Asn Gly Gly Cys Met His Met Lys Cys Pro
291          425          430          435
293 cag ccc cag tgc agg ctc gag tgg tgc tgg aac tgt ggc tgc gag tgg      1460
294 Gln Pro Gln Cys Arg Leu Glu Trp Cys Trp Asn Cys Gly Cys Glu Trp
295          440          445          450
297 aac cgc gtc tgc atg ggg gac cac tgg ttc gac gtg tagccagggc      1506
298 Asn Arg Val Cys Met Gly Asp His Trp Phe Asp Val
299          455          460          465
301 ggccggggcgc cccatcgcca catcctgggg gagcataccc agtgtctacc ttcattttct      1566
303 aattctcttt tcaaacacac acacacacgc gcgcgcgcgc acacacactc ttcaagtttt      1626
305 ttccaagtc caactacagc caaattgcag aagaaactcc tggatccctt tcactatgtc      1686
307 catgaaaaaac agcagagtaa aattacagaa gaagctcctg aatccctttc agtttgtcca      1746
309 cacaagacag cagagccatc tgcgacacca ccaacaggcg ttctcagcct ccggatgaca      1806
311 caaataccag agcacagatt caagtgaat ccatgtatct gtatgggtca ttctcacctg      1866
313 aattcgagac aggcagaatc agtagctgga gagagagttc tcacatttaa tatcctgcct      1926
315 ttaccttca gtaaaccacca tgaagatgcc attgacaagg tgtttctctg taaaatgaac      1986
317 tgcagtgggt tctccaaact agattcatgg cttaacagt aatgttctta tttaaatttt      2046
319 cagaaagcat ctattcccaa agaaccacag gcaatagtca aaaacatttg tttatcctta      2106
321 agaattccat ctatataaat cgcattaatc gaaataccaa ctatgtgtaa atcaacttgt      2166
323 cacaaagtga gaaattatga aagttaattt gaatgttgaa tgtttgaatt acaggaaga      2226
325 aatcaagtta atgtactttc attccctttc atgatttgca actttagaaa gaaattgttt      2286
327 ttctgaaagt atcaccaaaa aatctatagt ttgattctga gtattcattt tgcaacttgg      2346
329 agattttgct aatacatttg gctccactgt aaatttaata gataaagtgc ctataaagga      2406
331 aacacgttta gaaatgattt caaatgata ttcaatctta acaaaagtga acattattaa      2466
333 atcagaatct ttaaagagga gcctttccag aactaccaa atgaagacac gcccgactct      2526
335 ctccatcaga agggtttata cccctttggc acaccctctc tgtccaatct gcaagtcca      2586
337 gggagctctg cataccaggg gttcccagg agagaccttc tcttaggaca gtaaactcac      2646
339 tagaatattc cttatgttga catggattgg atttcagttc aatcaaactt tcagcttttt      2706
341 ttctagccat tcacaacaca atcaaaagat taacaacact gcatgcggca aaccgcatgc      2766
343 tcttaccac actacgcaga agagaaagta caaccactat cttttgttct acctgtattg      2826
345 tctgacttct caggaagatc gtgaacataa ctgaggcatc gagtctcact agcacatgga      2886
347 ggcccttttg gatttagaga ctgtaaatta ttaaateggc aacagggtct ctctttttag      2946
349 atgtagcact gaaa
352 <210> SEQ ID NO: 2
354 <211> LENGTH: 465
356 <212> TYPE: PRT

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358 <213> ORGANISM: Homo sapiens
360 <400> SEQUENCE: 2
362 Met Ile Val Phe Val Arg Phe Asn Ser Ser His Gly Phe Pro Val Glu
363 1 5 10 15
366 Val Asp Ser Asp Thr Ser Ile Phe Gln Leu Lys Glu Val Val Ala Lys
367 20 25 30
370 Arg Gln Gly Val Pro Ala Asp Gln Leu Arg Val Ile Phe Ala Gly Lys
371 35 40 45
374 Glu Leu Arg Asn Asp Trp Thr Val Gln Asn Cys Asp Leu Asp Gln Gln
375 50 55 60
378 Ser Ile Val His Ile Val Gln Arg Pro Trp Arg Lys Gly Gln Glu Met
379 65 70 75 80
382 Asn Ala Thr Gly Gly Asp Asp Pro Arg Asn Ala Ala Gly Gly Cys Glu
383 85 90 95
386 Arg Glu Pro Gln Ser Leu Thr Arg Val Asp Leu Ser Ser Ser Val Leu
387 100 105 110
390 Pro Gly Asp Ser Val Gly Leu Ala Val Ile Leu His Thr Asp Ser Arg
391 115 120 125
394 Lys Asp Ser Pro Pro Ala Gly Ser Pro Ala Gly Arg Ser Ile Tyr Asn
395 130 135 140
398 Ser Phe Tyr Val Tyr Cys Lys Gly Pro Cys Gln Arg Val Gln Pro Gly
399 145 150 155 160
402 Lys Leu Arg Val Gln Cys Ser Thr Cys Arg Gln Ala Thr Leu Thr Leu
403 165 170 175
406 Thr Gln Gly Pro Ser Cys Trp Asp Asp Val Leu Ile Pro Asn Arg Met
407 180 185 190
410 Ser Gly Glu Cys Gln Ser Pro His Cys Pro Gly Thr Ser Ala Glu Phe
411 195 200 205
414 Phe Phe Lys Cys Gly Ala His Pro Thr Ser Asp Lys Glu Thr Pro Val
415 210 215 220
418 Ala Leu His Leu Ile Ala Thr Asn Ser Arg Asn Ile Thr Cys Ile Thr
419 225 230 235 240
422 Cys Thr Asp Val Arg Ser Pro Val Leu Val Phe Gln Cys Asn Ser Arg
423 245 250 255
426 His Val Ile Cys Leu Asp Cys Phe His Leu Tyr Cys Val Thr Arg Leu
427 260 265 270
430 Asn Asp Arg Gln Phe Val His Asp Pro Gln Leu Gly Tyr Ser Leu Pro
431 275 280 285
434 Cys Val Ala Gly Cys Pro Asn Ser Leu Ile Lys Glu Leu His His Phe
435 290 295 300
438 Arg Ile Leu Gly Glu Glu Gln Tyr Asn Arg Tyr Gln Gln Tyr Gly Ala
439 305 310 315 320
442 Glu Glu Cys Val Leu Gln Met Gly Gly Val Leu Cys Pro Arg Pro Gly
443 325 330 335
446 Cys Gly Ala Gly Leu Leu Pro Glu Pro Asp Gln Arg Lys Val Thr Cys
447 340 345 350
450 Glu Gly Gly Asn Gly Leu Gly Cys Gly Phe Ala Phe Cys Arg Glu Cys
451 355 360 365
454 Lys Glu Ala Tyr His Glu Gly Glu Cys Ser Ala Val Phe Glu Ala Ser

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:7; Xaa Pos. 2,4,6,8,10,12,14

Seq#:8; Xaa Pos. 2,4,6,8,10,12,14

VERIFICATION SUMMARY

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L:68 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:54
L:512 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:498
L:1025 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:1155 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0